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PATENT APPLICATION: US/10/029,115DATE: 07/02/2002
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3 <110> APPLICANT: Luo, Ying
4 Fu, Alan C
5 Shen, Mary
7 <120> TITLE OF INVENTION: Novel Germinal Center Kinase Cell Cycle Protiens,
Compositions and
8 Methods of Use
10 <130> FILE REFERENCE: A-70229/RMS/DHR
12 <140> CURRENT APPLICATION NUMBER: US 10/029,115
13 <141> CURRENT FILING DATE: 2001-10-19
15 <160> NUMBER OF SEQ ID NOS: 15
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3951
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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27 cgggaccctg ctgggatctt tgagcttggt gaggtggctg gcaatggaac ctacggacag 120
29 gtgtacaagg gtccgcatgt caagacgggg cagctggctg ccatcaaggt catggatgtc 180
31 acggaggagc aggaggaaga gatcaaacag gagatcaaca tgctgaaaaa gtactctcac 240
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35 gaccagctct ggctggtgat ggagttctgt ggtgctggtt cagtgactga cctggtaaag 360
37 aacacaaaag gcaacgccct gaaggaggac tgtatcgctt atatctgcag ggagatcctc 420
39 aggggtcttg cccatctcca tgcccacaag gtgatccatc gagacatcaa ggggcagaat 480
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43 gaccgcaccg tgggcagacg gaacactttc attgggactc cctactggat ggctccagag 600
45 gtcacgcctt gtgatgagaa ccctgatgcc acctatgatt acaggagtga tatttggctt 660
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49 atgcgagccc tcttctctcat tctcgggaac cctccgccc ggtcaagtc caagaagtgg 780
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61 cagcaggaaa ataagagcaa ctcagaggct ttaaaacagc agcagcagct gcagcagcag 1140
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71 cagcggcagt cagaacgtct ccagaggcag ctgcagcagg agcatgccta cctcaagtcc 1440
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77 tgggcccag aggtagaaga gagaacaagg atgaacaagc agcagaactc tcccttggcc 1620
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85 cccgaccctg ccatccccgc acccactgcc acgcccagtg cccgaggagc tgtcatccgc 1860
87 cagaattcag accccaacct tgaaggacct ggccccagcc cgaatcccc agcctgggtc 1920
89 cgcccagata acgaggcccc acccaaggtg cctcagagga cctcatctat cgccactgcc 1980
91 cttaacacca gtggggcccg agggctcccg ccagcccagg cagtccgtgc cagacctgc 2040
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121 ggcactcggc tcgaccagct gcagtacgac gtgaggaagg gttctgtggt caacgtgaat 2940
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145 cccaacaccg acggcatgga gatgctgctg tgctacgagg acgaggggtg ctacgtcaac 3660
147 acgtacgggc gcatcattaa ggatgtgggt ctgcagtggg gggagatgcc tacttctgtg 3720
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151 gtggagacgg gccacctcga cggggtcttc atgcacaaac gagctcagag gctcaagttc 3840
153 ctgtgtgagc ggaatgacaa ggtgttttt gcctcagtc gctctggggg cagcagccaa 3900
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158 <210> SEQ ID NO: 2

159 <211> LENGTH: 1312

160 <212> TYPE: PRT

161 <213> ORGANISM: Homo sapiens

163 <400> SEQUENCE: 2

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165 Met Gly Asp Pro Ala Pro Ala Arg Ser Leu Asp Asp Ile Asp Leu Ser
166 1          5          10          15
169 Ala Leu Arg Asp Pro Ala Gly Ile Phe Glu Leu Val Glu Val Val Gly
170          20          25          30
173 Asn Gly Thr Tyr Gly Gln Val Tyr Lys Gly Arg His Val Lys Thr Gly
174          35          40          45

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177 Gln Leu Ala Ala Ile Lys Val Met Asp Val Thr Glu Asp Glu Glu Glu
178      50                      55                      60
181 Glu Ile Lys Gln Glu Ile Asn Met Leu Lys Lys Tyr Ser His His Arg
182 65                      70                      75                      80
185 Asn Ile Ala Thr Tyr Tyr Gly Ala Phe Ile Lys Lys Ser Pro Pro Gly
186                      85                      90                      95
189 Asn Asp Asp Gln Leu Trp Leu Val Met Glu Phe Cys Gly Ala Gly Ser
190                      100                      105                      110
193 Val Thr Asp Leu Val Lys Asn Thr Lys Gly Asn Ala Leu Lys Glu Asp
194                      115                      120                      125
197 Cys Ile Ala Tyr Ile Cys Arg Glu Ile Leu Arg Gly Leu Ala His Leu
198      130                      135                      140
201 His Ala His Lys Val Ile His Arg Asp Ile Lys Gly Gln Asn Val Leu
202 145                      150                      155                      160
205 Leu Thr Glu Asn Ala Glu Val Lys Leu Val Asp Phe Gly Val Ser Ala
206                      165                      170                      175
209 Gln Leu Asp Arg Thr Val Gly Arg Arg Asn Thr Phe Ile Gly Thr Pro
210                      180                      185                      190
213 Tyr Trp Met Ala Pro Glu Val Ile Ala Cys Asp Glu Asn Pro Asp Ala
214      195                      200                      205
217 Thr Tyr Asp Tyr Arg Ser Asp Ile Trp Ser Leu Gly Ile Thr Ala Ile
218      210                      215                      220
221 Glu Met Ala Glu Gly Ala Pro Pro Leu Cys Asp Met His Pro Met Arg
222 225                      230                      235                      240
225 Ala Leu Phe Leu Ile Pro Arg Asn Pro Pro Pro Arg Leu Lys Ser Lys
226                      245                      250                      255
229 Lys Trp Ser Lys Lys Phe Ile Asp Phe Ile Asp Thr Cys Leu Ile Lys
230                      260                      265                      270
233 Thr Tyr Leu Ser Arg Pro Pro Thr Glu Gln Leu Leu Lys Phe Pro Phe
234      275                      280                      285
237 Ile Arg Asp Gln Pro Thr Glu Arg Gln Val Arg Ile Gln Leu Lys Asp
238      290                      295                      300
241 His Ile Asp Arg Ser Arg Lys Lys Arg Gly Glu Lys Glu Glu Thr Glu
242 305                      310                      315                      320
245 Tyr Glu Tyr Ser Gly Ser Glu Glu Glu Asp Asp Ser His Gly Glu Glu
246                      325                      330                      335
249 Gly Glu Pro Ser Ser Ile Met Asn Val Pro Gly Glu Ser Thr Leu Arg
250                      340                      345                      350
253 Arg Glu Phe Leu Arg Leu Gln Gln Glu Asn Lys Ser Asn Ser Glu Ala
254      355                      360                      365
257 Leu Lys Gln Gln Gln Gln Leu Gln Gln Gln Gln Gln Arg Asp Pro Glu
258      370                      375                      380
261 Ala His Ile Lys His Leu Leu His Gln Arg Gln Arg Arg Ile Glu Glu
262 385                      390                      395                      400
265 Gln Lys Glu Glu Arg Arg Arg Val Glu Glu Gln Gln Arg Arg Glu Arg
266                      405                      410                      415
269 Glu Gln Arg Lys Leu Gln Glu Lys Glu Gln Gln Arg Arg Leu Glu Asp
270                      420                      425                      430
273 Met Gln Ala Leu Arg Arg Glu Glu Glu Arg Arg Gln Ala Glu Arg Glu

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274          435          440          445
277 Gln Glu Tyr Lys Arg Lys Gln Leu Glu Glu Gln Arg Gln Ser Glu Arg
278          450          455          460
281 Leu Gln Arg Gln Leu Gln Gln Glu His Ala Tyr Leu Lys Ser Leu Gln
282 465          470          475          480
285 Gln Gln Gln Gln Gln Gln Gln Leu Gln Lys Gln Gln Gln Gln Leu
286          485          490          495
289 Leu Pro Gly Asp Arg Lys Pro Leu Tyr His Tyr Gly Arg Gly Met Asn
290          500          505          510
293 Pro Ala Asp Lys Pro Ala Trp Ala Arg Glu Val Glu Glu Arg Thr Arg
294          515          520          525
297 Met Asn Lys Gln Gln Asn Ser Pro Leu Ala Lys Ser Lys Pro Gly Ser
298          530          535          540
301 Thr Gly Pro Glu Pro Pro Ile Pro Gln Ala Ser Pro Gly Pro Pro Gly
302 545          550          555          560
305 Pro Leu Ser Gln Thr Pro Pro Met Gln Arg Pro Val Glu Pro Gln Glu
306          565          570          575
309 Gly Pro His Lys Ser Leu Gln Asp Gln Pro Thr Arg Asn Leu Ala Ala
310          580          585          590
313 Phe Pro Ala Ser His Asp Pro Asp Pro Ala Ile Pro Ala Pro Thr Ala
314          595          600          605
317 Thr Pro Ser Ala Arg Gly Ala Val Ile Arg Gln Asn Ser Asp Pro Thr
318          610          615          620
321 Ser Glu Gly Pro Gly Pro Ser Pro Asn Pro Pro Ala Trp Val Arg Pro
322 625          630          635          640
325 Asp Asn Glu Ala Pro Pro Lys Val Pro Gln Arg Thr Ser Ser Ile Ala
326          645          650          655
329 Thr Ala Leu Asn Thr Ser Gly Ala Gly Gly Ser Arg Pro Ala Gln Ala
330          660          665          670
333 Val Arg Ala Arg Pro Arg Ser Asn Ser Ala Trp Gln Ile Tyr Leu Gln
334          675          680          685
337 Arg Arg Ala Glu Arg Gly Thr Pro Lys Pro Pro Gly Pro Pro Ala Gln
338          690          695          700
341 Pro Pro Gly Pro Pro Asn Ala Ser Ser Asn Pro Asp Leu Arg Arg Ser
342 705          710          715          720
345 Asp Pro Gly Trp Glu Arg Ser Asp Ser Val Leu Pro Ala Ser His Gly
346          725          730          735
349 His Leu Pro Gln Ala Gly Ser Leu Glu Arg Asn Arg Val Gly Ala Ser
350          740          745          750
353 Ser Lys Leu Asp Ser Ser Pro Val Leu Ser Pro Gly Asn Lys Ala Lys
354          755          760          765
357 Pro Asp Asp His Arg Ser Arg Pro Gly Arg Pro Ala Asp Phe Val Leu
358          770          775          780
361 Leu Lys Glu Arg Thr Leu Asp Glu Ala Pro Arg Pro Pro Lys Lys Ala
362 785          790          795          800
365 Met Asp Tyr Ser Ser Ser Ser Glu Glu Val Glu Ser Ser Glu Asp Asp
366          805          810          815
369 Glu Glu Glu Gly Glu Gly Gly Pro Ala Glu Gly Ser Arg Asp Thr Pro
370          820          825          830

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373 Gly Gly Arg Ser Asp Gly Asp Thr Asp Ser Val Ser Thr Met Val Val
374      835      840      845
377 His Asp Val Glu Glu Ile Thr Gly Thr Gln Pro Pro Tyr Gly Gly Gly
378      850      855      860
381 Thr Met Val Val Gln Arg Thr Pro Glu Glu Glu Arg Asn Leu Leu His
382 865      870      875      880
385 Ala Asp Ser Asn Gly Tyr Thr Asn Leu Pro Asp Val Val Gln Pro Ser
386      885      890      895
389 His Ser Pro Thr Glu Asn Ser Lys Gly Gln Ser Pro Pro Ser Lys Asp
390      900      905      910
393 Gly Ser Gly Asp Tyr Gln Ser Arg Gly Leu Val Lys Ala Pro Gly Lys
394      915      920      925
397 Ser Ser Phe Thr Met Phe Val Asp Leu Gly Ile Tyr Gln Pro Gly Gly
398      930      935      940
401 Ser Gly Asp Ser Ile Pro Ile Thr Ala Leu Val Gly Gly Glu Gly Thr
402 945      950      955      960
405 Arg Leu Asp Gln Leu Gln Tyr Asp Val Arg Lys Gly Ser Val Val Asn
406      965      970      975
409 Val Asn Pro Thr Asn Thr Arg Ala His Ser Glu Thr Pro Glu Ile Arg
410      980      985      990
413 Lys Tyr Lys Lys Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp
414      995      1000      1005
417 Gly Val Asn Leu Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu
418      1010      1015      1020
421 Asp Arg Ser Gly Gln Gly Lys Val Tyr Gly Leu Ile Gly Arg Arg
422      1025      1030      1035
425 Arg Phe Gln Gln Met Asp Val Leu Glu Gly Leu Asn Leu Leu Ile
426      1040      1045      1050
429 Thr Ile Ser Gly Lys Arg Asn Lys Leu Arg Val Tyr Tyr Leu Ser
430      1055      1060      1065
433 Trp Leu Arg Asn Lys Ile Leu His Asn Asp Pro Glu Val Glu Lys
434      1070      1075      1080
437 Lys Gln Gly Trp Thr Thr Val Gly Asp Met Glu Gly Cys Gly His
438      1085      1090      1095
441 Tyr Arg Val Val Lys Tyr Glu Arg Ile Lys Phe Leu Val Ile Ala
442      1100      1105      1110
445 Leu Lys Ser Ser Val Glu Val Tyr Ala Trp Ala Pro Lys Pro Tyr
446      1115      1120      1125
449 His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu Pro His Arg
450      1130      1135      1140
453 Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg Leu Lys
454      1145      1150      1155
457 Val Ile Tyr Gly Ser Ser Ala Gly Phe His Ala Val Asp Val Asp
458      1160      1165      1170
461 Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Val His Ile Gln Ser
462      1175      1180      1185
465 Gln Ile Thr Pro His Ala Ile Ile Phe Leu Pro Asn Thr Asp Gly
466      1190      1195      1200
469 Met Glu Met Leu Leu Cys Tyr Glu Asp Glu Gly Val Tyr Val Asn

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VERIFICATION SUMMARY

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